Protein families database of alignments and HMMs

ubiquitin

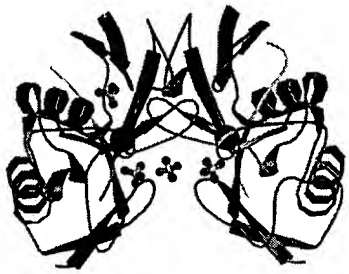

Figure 1: 1ndd
Signaling protein
Structure of nedd8

Key:

Domain	Chain	Start Residue	End Residue
ubiquitin	A	1	74
ubiquitin	B	101	174
ubiquitin	C	201	273
ubiquitin	D	301	373

The Swissprot/PDB mapping was provided by MSD

1a5r Display pdb

Accession number: **PF00240**

Ubiquitin family

Add Annotation

This family contains a number of ubiquitin-like proteins: SUMO (smt3 homologue) (see ULP1_YEAST), Nedd8 (see NED8_MOUSE), Elongin B (see Q15370), Rub1 (see Q9SHE7).

This family forms **structural complexes** with other Pfam families, to view them click here

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INTERPRO description (entry IPR000626)

Ubiquitin [MEDLINE:91274342], PUB00000768, PUB00000768 is a protein of seventy six amino acid residues, found in alleukaryotic cells and whose sequence is extremely well conserved from protozoan to vertebrates. It is widely known as a post-translational tag used to signal a protein's hydrolytic destruction. Other functions for ubiquitin, depend on its differential internal isopeptide linkages. In addition, several ubiquitin-like proteins have been discovered from genome-sequencing efforts, other structural studies, and genetic screens. These new data show that proteins with the ubiquitin domain are adaptable, transposable genetic elements, which have been appended to other genes and utilized for many different cellular functions, depending on the ubiquitin-like protein's identity, subcellular location, and method of covalent attachment. The post-translational ligation of proteins to members of the ubiquitin superfamily can signal many different fates for the target protein [Larsen and Wang (2002) J. Proteome Res. 1, 411-419.]

Ubiquitin is a globular protein, the last four C-terminal residues (Leu-Arg-Gly-Gly) extending from the compact structure to form a 'tail' important for its function. The latter is mediated by the covalent conjugation of ubiquitin to target proteins, by an isopeptide linkage between the C-terminal glycine and the epsilon amino group of lysine residues in the target proteins.

In most species, there are many genes coding for ubiquitin. However they can be classified into two classes. The first class produces polyubiquitin molecules consisting of exact head to tail repeats of ubiquitin. The number of repeats is variable. In the majority of polyubiquitin precursors, there is a final amino-acid after the last repeat. The second class of genes produces precursor proteins consisting of a single copy of ubiquitin fused to a C-terminal extension protein (CEP). There are two types of CEP proteins and both seem to be ribosomal proteins. There are a number of proteins which are evolutionary related to ubiquitin, including ubiquitin-like proteins from baculoviruses; mammalian proteins GDX, FAU and RAD23-related proteins; human spliceosome associated protein 114, proteins BAT3 and CKAP1/TFCB, and ubiquitin-like proteins SMT3A, SMT3C and SMT3B; yeast proteins RAD23, DK2 and SMT3; and Caenorhabditis elegans SMT3 and ubl-1 proteins.

For additional annotation, see the PROSITE document PDOC00271 [Expasy | SRS-UK | SRS-USA]

Alignment	Domain organisati n
Seed (95) Full (1365) Format Coloured alignment Get alignment View HMM logo Further alignment options here Help relating to Pfam alignments here	Seed (95) Full (1365) Context (3) As a Graphic As a Tree Zoom 0.5 pixels/aa. Bootstrap tree View Graphic NIFAS Applet To find out about the NIFAS tree-viewer, click here
Species Distribution	**Phylogenetic tree**
NEW! View alignments & domain organisation by species Tree depth : Show all levels View Species Tree	Seed (95) Full (1365) Download tree ATV Applet The trees were generated using Quicktree To find out more about ATV phylogenetic tree-viewer click here

Database References	
PDB You can find out how to set up Rasmol here	1bt0 A; 1; 73; PDB 2 Pfam Scop|Cath|Pfam CATH-PDBSUM SCOP-UK
PROSITE	PDOC00271 [Expasy | SRS-UK | SRS-USA]
PRINTS	PR00348
HOMSTRAD	UBQ
PFAMB	PB027829 PB039948 PB048702 PB068927 PB083641 PB088642 PB0927 PB096446
SYSTERS	ubiquitin
PANDIT	ubiquitin

Literature References
1. Structure of ubiquitin refined at 1.8 A resolution. Vijay-Kumar S, Bugg CE, Cook WJ; J Mol Biol 1987;194:531-544.
2. Structure of tetraubiquitin shows how multiubiquitin chains can be formed. Cook WJ, Jeffrey LC, Kasperek E, Pickart CM; J Mol Biol 1994;236:601-609.
3. Structure determination of

Pfam specific information	
Author of entry	Finn RD, Griffiths-Jones SR
Type definition	Domain
Alignment method of seed	Clustalw
Source of seed members	Prosite

HMMER build information		
	Pfam_ls [Download HMM]	**Pfam_fs** [Download HMM]
Gathering cutoff	25.5 25.5;	11.2 11.2

the small ubiquitin-r lat d modifi r SUMO-1. **Bayer P, Arndt A, Metzger S, Mahajan R, Melchior F, Jaenicke R, Becker J;** **J Mol Biol 1998;280:275-286.**		
4. Crystal structure of the human ubiquitin-like protein NEDD8 and interactions with ubiquitin pathway enzymes. **Whitby FG, Xia G, Pickart CM, Hill CP;** **J Biol Chem 1998;273:34983-34991.**		
	Trusted cutoff	26.2 26.1; 11.2 11.2
	Noise cutoff	25.2 25.2; 11.1 11.1
	Build method of HMM	hmmbuild -F HMM_ls SEED hmmcalibrate --seed 0 HMM_ls hmmbuild -f -F HMM_fs SEED hmmcalibrate --seed 0 HMM_fs

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